



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/779,476

DATE: 07/27/2004

TIME: 12:56:00

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Output Set: N:\CRF4\07272004\J779476.raw

3 <110> APPLICANT: Salmedix, Inc.  
 4 Leoni, Lorenzo M.  
 6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION AND TREATMENT OF  
 7 METHYLTHIOADENOSINE PHOSPHORYLASE DEFICIENT CANCERS  
 9 <130> FILE REFERENCE: 076936-0307942  
 11 <140> CURRENT APPLICATION NUMBER: 10/779,476  
 12 <141> CURRENT FILING DATE: 2004-02-13  
 14 <150> PRIOR APPLICATION NUMBER: 60/447,888  
 15 <151> PRIOR FILING DATE: 2003-02-14  
 17 <150> PRIOR APPLICATION NUMBER: 60/460,715  
 18 <151> PRIOR FILING DATE: 2004-04-04  
 20 <160> NUMBER OF SEQ ID NOS: 12  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 283  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
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 36 20 25 30  
 39 Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu Gly  
 40 35 40 45  
 43 Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg Gln  
 44 50 55 60  
 47 His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp Ala  
 48 65 70 75 80  
 51 Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys Gly  
 52 85 90 95  
 55 Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp Gln  
 56 100 105 110  
 59 Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly Ser  
 60 115 120 125  
 63 His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro Phe  
 64 130 135 140  
 67 Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu Gly  
 68 145 150 155 160  
 71 Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro Arg  
 72 165 170 175  
 75 Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala Asp  
 76 180 185 190  
 79 Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu Ala



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84          210          215          220
87 Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr Leu
88 225          230          235          240
91 Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile Pro
92          245          250          255
95 Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
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105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
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115 gcatgatcca gaaattttag aaggaagaac tgaaaaatat gtggatactc catttggcaa 240
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121 tttgaaggaa gagggctgta cacatgtcat agtgaccaca gcttgtggct ccttgaggga 420
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131 ggcagaaagc ttcattgttc gcacctgggg ggcgatgtt atcaacatga ccacagttcc 720
133 agaggtggtt cttgctaagg aggctggaat ttgttacgca agtatcgcca tggcgacaga 780
135 ttatgactgc tggaaggagc acgaggaagc agtttcggtg gaccgggtct taaagaccct 840
137 gaaagaaaac gctaataaag ccaaaagctt actgctcact accatacctc agatagggtc 900
139 cacagaatgg tcagaaaccc tccataacct gaagaatatg gcccgatttt ctgttttatt 960
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169 ctgggataat ttttattttc tttgaatctt tctgtgtctt cacatttttc tacagtgaat 1860
171 ataatacaat agtaaaaggc cgtaaaaata aaagtggatt tagaaaagatc cagttcttga 1920
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175 taagggaggtt acatctttat tctgctaaag aagaggatca ttgatttctg tacagtcaga 2040
177 acagtacttg ggtgtgcaac agctttctga gaaaagctag gtgtataata gtttaactga 2100
179 aagtttaact atttaaaaga ctaaatgcac attttatggg atctgatatt ttaaaaagta 2160
181 atgtgagctt ctccttttta tgagttaaat tttttatac gagttggtaa tttgtgcctt 2220
183 ttaataaagt ggaagcttgc tttttaaaaa aaaaaaaaaa gcggaattc 2269

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186 &lt;210&gt; SEQ ID NO: 3

187 &lt;211&gt; LENGTH: 156

188 &lt;212&gt; TYPE: PRT

189 &lt;213&gt; ORGANISM: Homo sapiens

191 &lt;400&gt; SEQUENCE: 3

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194 1 5 10 15

197 Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu

198 20 25 30

201 Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro

202 35 40 45

205 Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu

206 50 55 60

209 Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg

210 65 70 75 80

213 Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val

214 85 90 95

217 Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg

218 100 105 110

221 Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg

222 115 120 125

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233 &lt;210&gt; SEQ ID NO: 4

234 &lt;211&gt; LENGTH: 1218

235 &lt;212&gt; TYPE: DNA

236 &lt;213&gt; ORGANISM: Homo sapiens

238 &lt;400&gt; SEQUENCE: 4

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241 tcctccgagc actcgctcac ggctcccct tgcttgaaaa gataccgcgg tccctccaga 120

243 ggatttgagg gacagggctc gagggggctc ttccgccagc accggaggaa gaaagaggag 180

245 gggctggctg gtcaccagag ggtggggcgg accgctgctg ctccggcggt gcggagaggg 240

247 ggagagcagg cagcggggcg cggggagcag catggagccg gcggcgggga gcagcatgga 300

249 gccttcggct gactggctgg ccacggccgc ggcccggggt cgggtagagg aggtgcgggc 360

251 gctgctggag gcgggggcgc tgcccaacgc accgaatagt tacggtcggg gcccgatcca 420

253 ggtcatgatg atgggcagcg cccgagtggc ggagctgctg ctgctccacg gcgcggagcc 480

255 caactgcgcc gaccccgcca ctctcacccg acccgtgcac gacgctgccc gggagggcctt 540

257 cctggacacg ctggtggtgc tgcaccgggc cggggcgcgg ctggacgtgc gcgatgcctg 600

259 gggccgtctg cccgtggacc tggctgagga gctgggcat cgcgatgtcg cacggtacct 660

261 gcgcgcggct gcggggggca ccagaggcag taacctatgc cgcgatagatg ccgcggaagg 720

263 tccctcagac atccccgatt gaaagaacca gagaggctct gagaaacctc gggaaaactta 780

265 gatcatcagt caccgaaggt cctacagggc cacaactgcc cccgccacaa cccaccccg 840

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269 atatgccttc cccactacc gtaaagtgtcc atttatatca ttttttataat attccttataa      960
271 aaatgtaaaa aagaaaaaca ccgcttctgc cttttcactg tgttgagggtt ttctggagtg      1020
273 agcactcacg ccctaagcgc acattcatgt gggcatttct tgcgagcctc gcagcctccg      1080
275 gaagctgtcg acttcatgac aagcattttg tgaactaggg aagctcaggg gggttactgg      1140
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283 <211> LENGTH: 173
284 <212> TYPE: PRT
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294 20 25 30
297 Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val
298 35 40 45
301 Thr Leu Arg Ile Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe
302 50 55 60
305 Val Val His Ile Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala
306 65 70 75 80
309 Pro Ala Ala Val Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu
310 85 90 95
313 Gly Gln Gln Pro Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg
314 100 105 110
317 Pro Ser Gly Gly Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg
318 115 120 125
321 Arg Pro Arg His Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly
322 130 135 140
325 Leu Pro Gly His Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly
326 145 150 155 160
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330 165 170
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334 <211> LENGTH: 1275
335 <212> TYPE: DNA
336 <213> ORGANISM: Homo sapien
338 <400> SEQUENCE: 6
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343 gggcgcgctc aggaaggcg ggtgcgcgcc tgcggggcgg agatgggcag gggcggtgc      180
345 gtgggtccca gtctgcagtt aagggggcag gagggtgcgt gctcacctct ggtgccaaag      240
347 ggcggcgtag cggctgccga gctcggccct ggaggcggcg agaacaatgg gcgcaggttc      300
349 ttggtgaccc tccggttcg gcgcgcgtgc ggcccgcgcg gaggtaggggt tttcgtgggt      360
351 cacatcccgc ggctcacggg ggagtgggca gcgccagggg cgcgcgcgcg tgtggccctc      420
353 gtgctgatgc tactgaggag ccagcgtcta gggcagcagc cgcttcctag aagaccaggt      480
355 catgatgatg ggcagcgcgc gaggggcgga gctgctgctg ctccacggcg cggagcccaa      540
357 ctgcgccgac cccgccactc tcaccgacc cgtgcacgac gctgcccggg agggcttct      600

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363 cgcggctgcg gggggcacca gaggcagtaa ccatgcccgc atagatgccg cgggaaggcc 780
365 ctacagacatc cccgattgaa agaaccagag aggcctctgag aaacctcggg aaacttagat 840
367 catcagtcac cgaaggctcct acagggccac aactgcccc gccacaaccc accccgcttt 900
369 cgtagttttc atttagaaaa tagagctttt aaaaatgtcc tgccttttaa cgtagatata 960
371 tgccttcccc cactaccgta aatgtccatt tatatcattt tttatatatt cttataaaaa 1020
373 tgtaaaaaaag aaaaacaccg cttctgcctt ttcaactgtg tggagttttc tggagtgage 1080
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377 gctgtcgact tcatgacaag cattttgtga actagggaag ctcagggggg ttactggctt 1200
379 ctcttgagtc aactgctag caaatggcag aaccaaagct caaataaaaa taaaataatt 1260
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384 &lt;210&gt; SEQ ID NO: 7

385 &lt;211&gt; LENGTH: 105

386 &lt;212&gt; TYPE: PRT

387 &lt;213&gt; ORGANISM: Homo sapiens

389 &lt;400&gt; SEQUENCE: 7

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396 20 25 30
399 Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
400 35 40 45
403 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val
404 50 55 60
407 Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
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412 85 90 95
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416 100 105

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421 &lt;212&gt; TYPE: DNA

422 &lt;213&gt; ORGANISM: Homo sapiens

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429 ccgagtggcg gagctgctgc tgctccacgg cgcggagccc aactgcgcgc accccgccac 180
431 tctcaccgga cccgtgcacg acgctgcccg ggagggcttc ctggacacgc tgggtggtgct 240
433 gcaccggggc ggggcgcggc tggacgtgcg cgatgcctgg ggccgtctgc ccgtggacct 300
435 ggctgaggag ctgggccatc gcgatgtcgc acggtacctg cgcgcggctg cggggggcac 360
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439 aaagaaccag agaggctctg agaaacctcg ggaaacttag atcatcagtc accgaaggtc 480
441 ctacagggcc acaactgccc ccgccacaac ccaccccgct ttcgtagttt tcatttagaa 540
443 aatagagctt ttaaaaatgt cctgcctttt aacgtagata taagccttcc ccactaccg 600
445 taaatgtcca tttatatcat tttttatata ttcttataaa aatgtaaaaa agaaaaacac 660
447 cgcttctgcc ttttactgt gttggagttt tctggagtga gcactcacgc cctaagcgca 720
449 cattcatgtg ggcatttctt gcgagcctcg cagcctccgg aagctgtcga cttcatgaca 780

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**VERIFICATION SUMMARY**

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